

1 gcgtctccac ccctcagcg
61 agcgggcgtg aaggcgcgag
121 gagttagat acccttcaa
181 AAGAAAAAA GGAAGACGAT
241 AACGTGTTCA TTGGAGTCT
301 GAAAATGGG GCACACTCAC
361 AGAGGCTTTG GCTTGTTC
421 CGACCACATA AGGTGGATGG
481 TCTGTAAAGC CTGGGGCCA
541 GATACAGAAG AAATAATA
601 GAAGTCATGG AACACAGACA
661 GATCACGATA CAGTTGATA
721 TGCGAAGATA AAAAAGCACT
781 CGTGGGGGTG GTTCAGGCAA
841 TTTGCCAG GAGGAAACTT
901 GGGAGCAGAG GAAGCTTGG
961 TATGGAGGTG GTCCCTGGCTA
1021 TATGAAAC CAGGTGGTGG
1081 GGAGGCAATT TTGGAGTGG
1141 TACAGTGGAC AGCAGCAGTC
1201 AAAGAATTCAAG GCAGTCCTA
1261 GGTGGTAGAA GATTCTaaaa
1321 gagcggaggag ttgtcaggaa
1381 gaggaaactgt aaaatctgc
1441 gcttaaacag gaaacccttc
1501 gctattgggt aatgtcaatgt
1561 agcttgcgtt ttcttttc
1621 ttgttgttagt ggtaaccaggaa
1681 aaaaaaaaaaa

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ctgaacgcgtc gcacggttt cttagatcta aagaaggcc
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CAGCAGCAGG CATGAGCTA AGGAGCCAGA GCAGTTGAGA
GAGCTTCGAG ACCGAGGTG ATAGCTTGAG ACAGCACTTT
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TTACTCTTGC GTGGAAGAGG TGGATGCGGC CATGAGCGCT
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TCTCACAGTA AAGAAAATAT TTGTGTTGTTG CATTAAAGAA
AAGGGGGTAC TTTGAAACAT ATGCCAAGAT CGAAACGATA
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AATTTGTTG CAGAAATAC ATACTATAAA TGGTCATAA
CTCAAAACAA GAGATCGAGA CTGGCAGCTC TCAGAGAGGT
CTTCAATGGGT CGTGGAAATT TTGGAGGTGC TGGAGGAAAC
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TGCCAGCAGA GGGGGTTATG GTGCTGGTGG AGGACCAGGA
ATATGGAGGT GGAGGGAGGAG GATATGGTGG CTACAAATGAA
TAATTATGGA GGCAGTGGAA ACTACATGA CTTGGTAA
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cgatgatcca tagtcagaaa agttactgc
ttgtcaggaa ctgtcatgc cacagtttgc aaaaagagca
atgtcgttta gatgtacatc ctgaggctt tatactgtt
tttttttttcccattacat caggttatatt gccctgtaaa
taaggaattt ttggctttc aaaaaaaaaaa

Fig. 1a

CHKA1	- MAAIKEEREVEDYKRKRKTISTGHEPKPEPQLRKLFIGGLS FETTDDSLR	- 50
HUMA1	- M-----SKSESPKEPEPQLRKLFIGGLS FETTDESLR	- 31
CHKA1	- <u>EQFEKWGT</u> LTD CVVMRD PQT KRSRGFGFVT YSCVEVDAAMSARPHKVDG	- 100
HUMA1	- SHFEQWGT LTD <u>CVVMRD</u> PNT KRSRGFGFVT YATVEEVDAAMNARPHKVDG	- 81
CHKA1	- RVVEPKRAVS REDSV KPGAH LTVKKI FVGGI KEDTEEY NLRGYFETYGKI	- 150
HUMA1	- RVVEPKRAVS REDS QRP GAHLT VKKI FVGGI KEDTE EEHLD RDYF EQY GKI	- 131
CHKA1	- ETIEVMEDRQSGK <u>KRGFA</u> FVT FDDHD TVDKIVVQKYHT INGHN CEDKKAL	- 200
HUMA1	- EVIEIMTD RGS GK <u>KRGFA</u> FVT FDDHD SV DVKIV QKYHT VNGHN CEVRKAL	- 181
CHKA1	- SKQEMQTASS- QRGRGGGS GNFMGRGNFGGGGG-----NFGRGGNF GG	- 242
HUMA1	- SKQEMASASSSQ RGRSGS -----GNFGGGRRGGFGGGNDNFGRGGNF SG	- 224
CHKA1	- RGGYGGGGGGGGSRGS FGGGD G YNG FG DGGNY GGGP GY GS RGGY GGGGP	- 292
HUMA1	- RGG F GGGS RGGGG Y GG S--- G D G Y N G F GN D G-----	- 252
CHKA1	- GYGNPGGGYGGGGGGYGGYNEGGNF GGG NYGGSGNY NDF GN Y SG QQQ S NY	- 342
HUMA1	- ----- N F GGGG S Y NDF GN Y NN Q S- SN F	- 273
CHKA1	- GPMKGGGS F GG RSSG S PY GGG-----Y GSG S G GGY G - GRRF	- 378
HUMA1	- GPMKGG- N F GGR SSG-PYGGGG QY F AKP R N Q GGY GGSSSSSSY GS GRRF	- 320

Fig. 1b

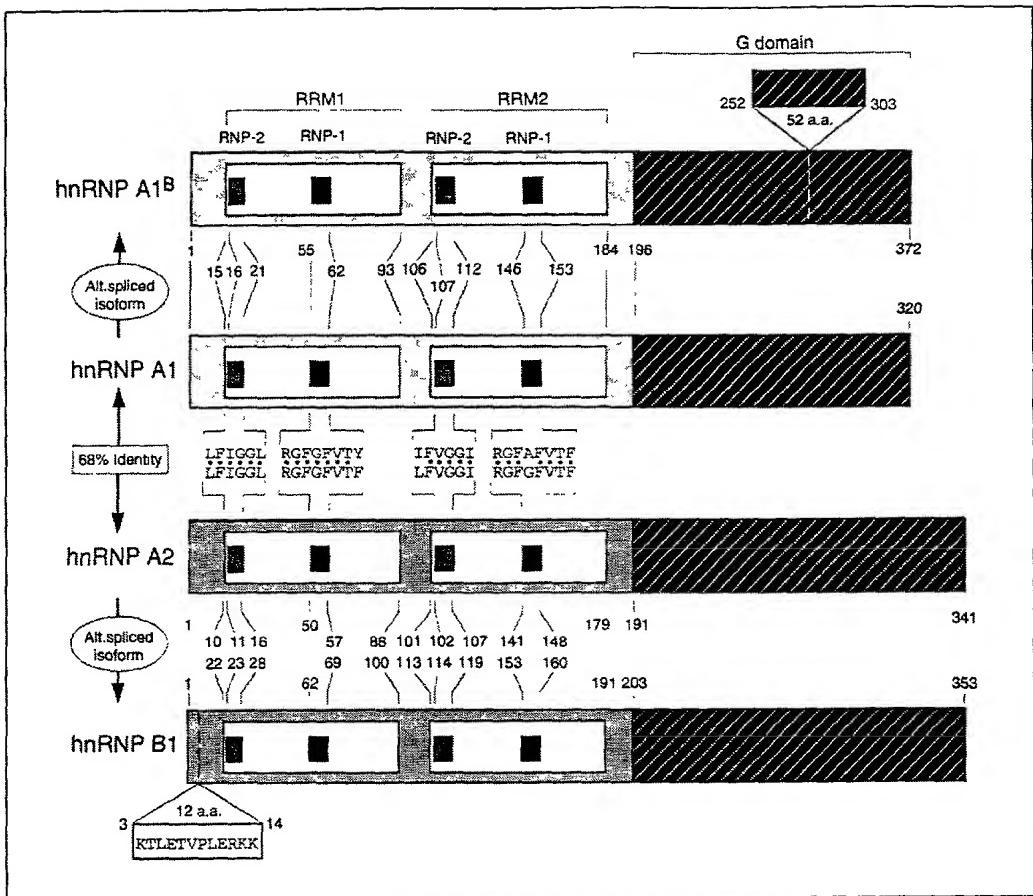


Fig. 2

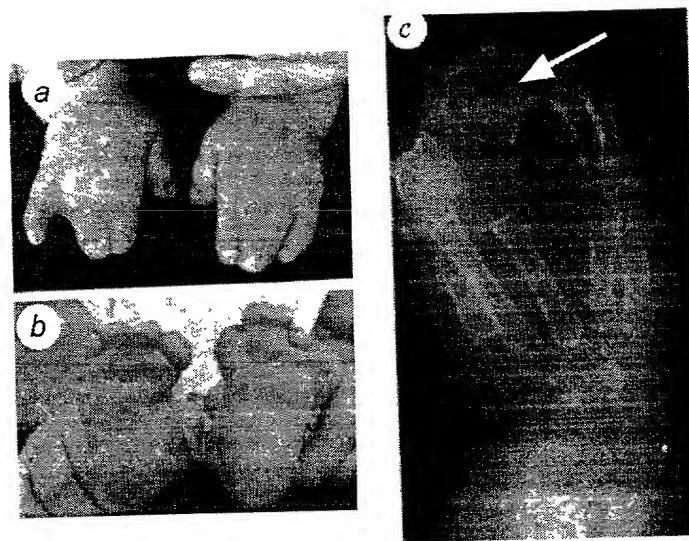


Fig. 3

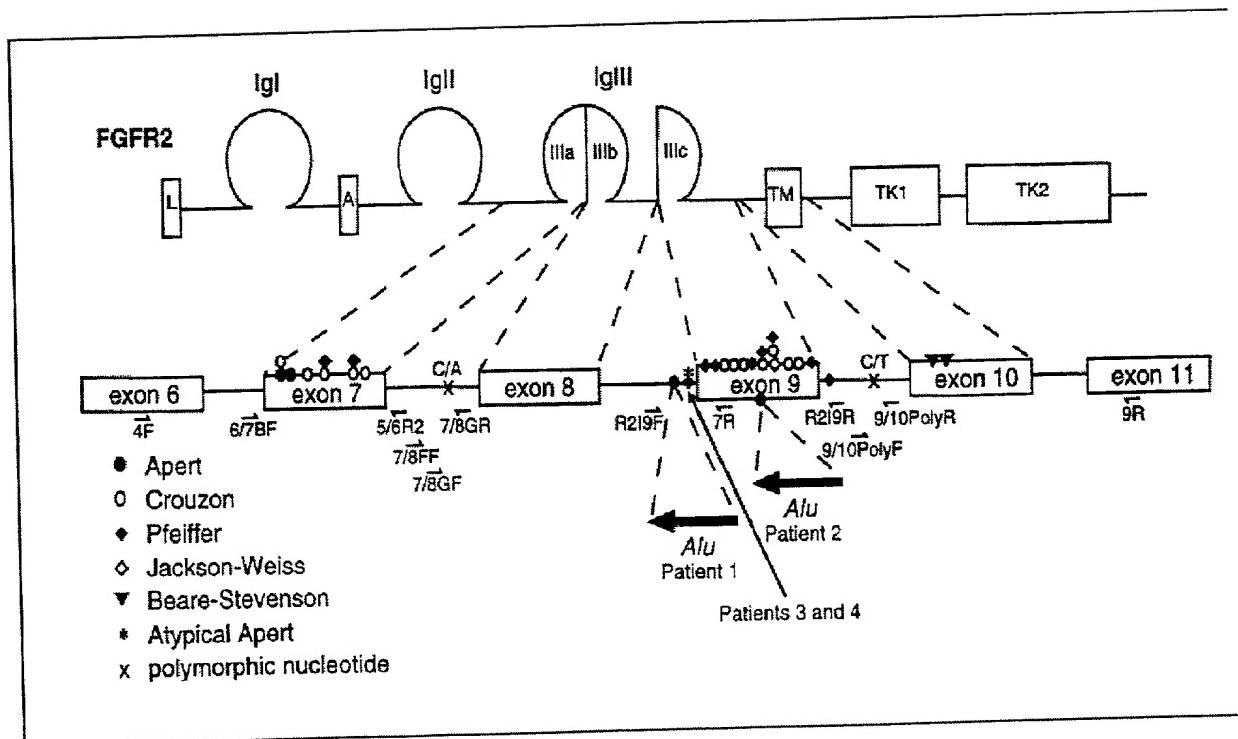


Fig. 4

Fig. 5

